

## SEQUENCE LISTING

<110> OriGene Technologies, Inc  
 <120> Human EphA6 Gene and Polypeptide  
 <130> OGT 16U 102 R1  
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 <170> PatentIn version 3.0  
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16U 102 R1.ST25

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gga att aaa act tac att gat cca gat aca tat gaa gac cca tcc cta Gly Ile Lys Thr Tyr Ile Asp Pro Asp Thr Tyr Glu Asp Pro Ser Leu 605 610 615		1936
gca gtc cat gaa ttt gca aag gag att gat ccc tca aga att cgt att Ala Val His Glu Phe Ala Lys Glu Ile Asp Pro Ser Arg Ile Arg Ile 620 625 630		1984
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aaaa ggt ggc cac atg gat cgg caa aga aga gat ttt cta aga gaa gct Lys Gly Gly His Met Asp Arg Gln Arg Arg Asp Phe Leu Arg Glu Ala 670 675 680		2128
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810	815	820	825
gat cca gaa gct gct tat aca aca act ggt gga aaa atc ccc ata agg Asp Pro Glu Ala Ala Tyr Thr Thr Gly Gly Lys Ile Pro Ile Arg			2608
830	835	840	
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845	850	855	
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925	930	935	
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940	945	950	
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955	960	965	
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970	975	980	985
ggg ttt aca aca ttt gac ctg att tca aga atg agc att gat gac att Gly Phe Thr Thr Phe Asp Leu Ile Ser Arg Met Ser Ile Asp Asp Ile			3088
990	995	1000	
aga aga att gga gtc ata ctt att gga cac cag aga cga ata gtc Arg Arg Ile Gly Val Ile Leu Ile Gly His Gln Arg Arg Ile Val			3133
1005	1010	1015	
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caaccagat tttaaaatca tgctacataa atccgttctg aataacctgc aactaaaacc			3406
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Glu His Asn Arg Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Glu  
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Pro Asn Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Arg Asp Ala  
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Ala Gln Lys Ile Tyr Val Glu Met Lys Phe Thr Leu Arg Asp Cys Asn  
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Ser Ile Pro Trp Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Phe  
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Tyr Met Glu Ser Asp Glu Ser His Gly Ile Lys Phe Lys Pro Asn Gln  
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Lys Asp Pro Pro Ser Met Ala Cys Thr Arg Pro Pro Ser Ala Pro Arg  
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Cys Lys Lys Cys Gly Leu Asp Thr Ser Gln Cys Glu Asp Cys Gly Gly  
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Ala Ile Thr Val Thr Asp Gln Asp Ala Pro Ser Leu Ile Gly Val  
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Val Arg Lys Asp Trp Ala Ser Gln Asn Ser Ile Ala Leu Ser Trp Gln  
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Tyr Glu Lys Glu His Glu Gln Leu Thr Tyr Ser Ser Thr Arg Ser Lys  
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Phe His Ile Arg Val Arg Thr Ala Thr Gly Tyr Ser Gly Tyr Ser Gln  
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Leu Gln Asn Gly His Leu Arg Phe Pro Gly Ile Lys Thr Tyr Ile Asp  
595 600 605

Pro Asp Thr Tyr Glu Asp Pro Ser Leu Ala Val His Glu Phe Ala Lys  
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Glu Ile Asp Pro Ser Arg Ile Arg Ile Glu Arg Val Ile Gly Ala Gly  
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Glu Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Thr Pro Gly Lys Arg  
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Glu Ile Pro Val Ala Ile Lys Thr Leu Lys Gly Gly His Met Asp Arg  
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Gln Arg Arg Asp Phe Leu Arg Glu Ala Ser Ile Met Gly Gln Phe Asp  
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His Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr Lys Arg Ser Phe  
690 695 700

Pro Ala Ile Gly Val Glu Ala Phe Cys Pro Ser Phe Leu Arg Ala Gly  
705 710 715 720

Phe Leu Asn Ser Ile Gln Ala Pro His Pro Val Pro Gly Gly Ser  
725 730 735

Leu Pro Pro Arg Ile Pro Ala Gly Arg Pro Val Met Ile Val Val Glu  
740 745 750

Tyr Met Glu Asn Gly Ser Leu Asp Ser Phe Leu Arg Lys His Asp Gly  
755 760 765

His Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ser  
770 775 780

Gly Met Lys Tyr Leu Ser Asp Met Gly Tyr Val His Arg Asp Leu Ala  
785 790 795 800

Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp  
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Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr  
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Thr Thr Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile  
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Ala Tyr Arg Lys Phe Ser Ser Ala Ser Asp Ala Trp Ser Tyr Gly Ile  
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Val Met Trp Glu Val Met Ser Tyr Gly Glu Arg Pro Tyr Trp Glu Met  
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Trp Gln Lys Glu Arg Asn His Arg Pro Lys Phe Thr Asp Ile Val Ser  
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Gln Tyr Lys Asn Asn Phe Val Ala Ala Gly Phe Thr Thr Phe Asp Leu  
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Ile Ser Arg Met Ser Ile Asp Asp Ile Arg Arg Ile Gly Val Ile Leu  
 995 1000 1005

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Gln Val Val Leu Leu Asp Thr Thr Thr Val Met Gly Glu Leu Gly Trp  
35 40 45

Lys Thr Tyr Pro Leu Asn Gly Trp Asp Ala Ile Thr Glu Met Asp Glu  
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His Asn Arg Pro Ile His Thr Tyr Gln Val Cys Asn Val Met Glu Pro  
65 70 75 80

Asn Gln Asn Asn Trp Leu Arg Thr Asn Trp Ile Ser Arg Asp Ala Ala  
85 90 95

Gln Lys Ile Tyr Val Glu Met Lys Phe Thr Leu Arg Asp Cys Asn Ser  
100 105 110

Ile Pro Trp Val Leu Gly Thr Cys Lys Glu Thr Phe Asn Leu Tyr Tyr  
115 120 125

Ile Glu Ser Asp Glu Ser His Gly Thr Lys Phe Lys Pro Ser Gln Tyr  
130 135 140

Ile Lys Ile Asp Thr Ile Ala Ala Asp Glu Ser Phe Thr Gln Met Asp  
145 150 155 160

Leu Gly Asp Arg Ile Leu Lys Leu Asn Thr Glu Ile Arg Glu Val Gly  
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Pro Ile Glu Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala  
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Cys Ile Ala Leu Val Ser Val Arg Val Phe Tyr Lys Lys Cys Pro Phe  
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Thr Val Arg Ser Leu Ala Met Phe Pro Asp Thr Ile Pro Arg Val Asp  
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Ser Ser Ser Leu Val Glu Val Arg Gly Ser Cys Val Lys Ser Ala Glu  
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Glu Arg Asp Thr Pro Lys Leu Tyr Cys Gly Ala Asp Gly Asp Trp Leu  
245 250 255

Val Pro Leu Gly Arg Cys Ile Cys Ser Thr Gly Tyr Glu Glu Ile Glu  
260 265 270

Gly Ser Cys His Ala Cys Arg Pro Gly Phe Tyr Lys Ala Phe Ala Gly  
275 280 285

Asn Thr Lys Cys Ser Lys Cys Pro Pro His Ser Ser Thr Tyr Val Glu  
290 295 300

Ala Thr Ser Val Cys His Cys Glu Lys Gly Tyr Phe Arg Ala Glu Lys  
305 310 315 320

Asp Pro Pro Ser Met Ala Cys Thr Arg Pro Pro Ser Ala Pro Arg Asn  
325 330 335

Val Ala Phe Asn Ile Asn Glu Thr Ala Leu Ile Leu Glu Trp Ser Pro  
340 345 350

Pro Ser Asp Thr Gly Arg Lys Asp Leu Thr Tyr Ser Val Ile Cys  
355 360 365

Lys Lys Cys Gly Leu Asp Thr Thr Gln Cys Glu Asp Cys Gly Gly  
370 375 380

Leu Arg Phe Ile Pro Arg His Thr Gly Leu Ile Asn Asn Ser Val Val  
385 390 395 400

Val Leu Asp Phe Val Ser His Val Asn Tyr Thr Phe Glu Ile Glu Ala  
405 410 415

Met Asn Gly Val Ser Glu Leu Ser Ile Ser Pro Lys Pro Phe Thr Ala

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Arg Lys Asp Trp Ala Ser Gln Asn Ser Leu Ala Leu Ser Trp Gln Ala		
450	455	460
Pro Ala Phe Ser Asn Gly Ala Ile Leu Asp Tyr Glu Thr Lys Tyr Tyr		
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Glu Lys Glu His Glu Gln Leu Thr Tyr Ser Ser Thr Arg Ser Lys Ala		
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Pro Ser Val Ile Val Thr Gly Leu Lys Pro Ala Thr Thr Tyr Ile Phe		
500	505	510
His Ile Arg Val Arg Thr Ala Thr Gly Tyr Ser Gly Tyr Ser Gln Lys		
515	520	525
Phe Glu Phe Glu Thr Gly Asp Glu Thr Ser Asp Met Ala Ala Glu Gln		
530	535	540
Gly Gln Ile Leu Val Ile Ala Thr Ala Ala Val Gly Gly Phe Thr Leu		
545	550	555
Leu Val Ile Leu Thr Leu Phe Phe Leu Ile Thr Gly Arg Cys Gln Trp		
565	570	575
Tyr Ile Lys Ala Lys Met Lys Ser Glu Glu Lys Arg Arg Thr His Leu		
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Gln Asn Gly His Leu Arg Phe Pro Gly Ile Lys Thr Tyr Ile Asp Pro		
595	600	605
Asp Thr Tyr Glu Asp Pro Ser Leu Ala Val His Glu Phe Ala Lys Glu		
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Ile Asp Pro Ser Arg Ile Arg Ile Glu Arg Val Ile Gly Ala Gly Glu		
625	630	635
Phe Gly Glu Val Cys Ser Gly Arg Leu Lys Thr Pro Gly Lys Arg Glu		
645	650	655
Ile Pro Val Ala Ile Lys Thr Leu Lys Gly Gly His Met Asp Arg Gln		
660	665	670
Arg Arg Asp Phe Leu Arg Glu Ala Ser Ile Met Gly Gln Phe Asp His		
675	680	685
Pro Asn Ile Ile Arg Leu Glu Gly Val Val Thr Lys Arg Ser Phe Pro		
690	695	700
Ala Ile Gly Val Glu Ala Phe Cys Pro Ser Phe Leu Arg Ala Gly Phe		
705	710	715
Leu Asn Gly Ile Gln Ala Pro His Pro Val Thr Ala Gly Ser Leu		
725	730	735
Pro Pro Arg Ile Pro Ala Gly Arg Pro Val Met Ile Val Val Glu Tyr		
740	745	750
Met Glu Asn Gly Ser Leu Asp Ser Phe Leu Arg Lys His Asp Gly His		
755	760	765
Phe Thr Val Ile Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ser Gly		
770	775	780
Met Lys Tyr Leu Ser Asp Met Gly Tyr Val His Arg Asp Leu Ala Ala		
785	790	795
Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe		
805	810	815

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Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Ala Tyr Thr Thr  
820 825 830

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Tyr Lys Ser Asn Phe Met Ala Ala Gly Phe Thr Thr Phe Asp Leu Ile  
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